

0590
0124

Page 1 of 7



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/826,581

DATE: 01/26/2002
TIME: 16:32:24

Input Set : A:\11145-007001.txt
Output Set: N:\CRF3\01262002\I826581.raw

ENTERED

4 <110> APPLICANT: Andersson, Leif
5 Luthman, L. Holger
6 Marklund, Stefan
8 <120> TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3
SUBUNIT
10 <130> FILE REFERENCE: 11145-007001
12 <140> CURRENT APPLICATION NUMBER: US 09/826,581
13 <141> CURRENT FILING DATE: 2001-04-05
15 <150> PRIOR APPLICATION NUMBER: US 60/195,665
16 <151> PRIOR FILING DATE: 2000-04-07
18 <160> NUMBER OF SEQ ID NOS: 14
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 821
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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30 agattatccg gtgcgcctt ccctcccaag caaccccccag cttcaggcc ttagcagct 180
31 gagcaaatgg gggccctcc ctctcattgc ctgacaccca atcagagaga aaccgatcct 240
32 ggcagggcag ggtgcgggg gccggggccca gaatagtgca gcccagccac agtgtcgac 300
33 acttgctctc atgtggctcg gggctggcca catggagccc gggctggagc acgcactgcg 360
34 cagggtatgg gggtcccaagg ggagccggag ccggggcagc tgaggccaga agattgagcg 420
35 cacgggctgt gaatgtgtgt gtggggctgt gtgtcttctg gtgtgtgttt ggtctggatt 480
36 ttctcgtgaa tatgggcatt tcgtatgtttt ggcataatgta ttgtgagtgt gtgtgtttct 540
37 gtgtgcctgg gaggttttgg atgtgtgtgt ttctgtgtgt gtgtgtgtat ggctgcattgt 600
38 ctgtgtatgg ctgtgtctg agcgtgtgtt ttgggtgtca tgggtgtgtt ggcgtgtgtt 660
39 cagggagaag gggtttggga atgttaaggca ctttccccac tccttcagaa actcttctcc 720
40 ccacagaccc ttccctggag cagccttggg gttctgagc atcaaggtag ggagaatgcc 780
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51 ttagatggac aaggcagaag tgggtggagg aaggggagcc accaggtcaq ggggaagggtg 180
52 aggccaaggc cagttctggg gaggtgggg ccaggggagt gggaaatccc agaggagcct 240
53 gggctggtc tctacctcag ttccctccat aacacagagt tgacccaaac cttcatctt 300
54 tggcctcagt ctccctacat agtagagaac aaggcactgc atgtccagag gccagcatgg 360
55 ccaactcaga aagatggac agagccacta cctggggcga ctctcaggc agccctcac 420
56 ctgcaaata ggcacagca tccaggcttc ccactgtgc tggatgtat atggcgacag 480

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57 cagatgagaa	cgtgctttgg	aagatggagt	tactgtcctc	ttccccctcct	cccccaaaca	540
58 ggtcccccgt	ccaggccagc	tgctgagtcc	accgggctgg	aggccacatt	ccccaaagacc	600
59 acacccttgg	ctcaagctga	tcctgccggg	gtggcactc	caccaacagg	gtgggactgc	660
60 ctccccctcg	actgtacagc	ctcagctgca	ggctccagca	cagatgatgt	ggagctggcc	720
61 acggagttcc	cagccacaga	ggcctgggag	tgtgagctag	aaggcctgt	ggaagagagg	780
62 cctgccctgt	gcctgtcccc	gcaggcccc	tttccaagc	tgggctggga	tgacgaactg	840
63 cggaaaccgg	gcgcccagat	ctacatgcgc	ttcatgcagg	gacacacctg	ctacatgcgc	900
64 atggcaacta	gctccaagct	agtcatctc	gacaccatgc	tggaggttag	gccacggctc	960
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74 coctctatgg	gacagcaaga	agcagagctt	tgtgggttag	gagaggctgg	ggaggtgaag	120
75 ggagatggag	gaggtgaggg	ggagatcttg	tacggttgtt	ctggggctga	tctctgatat	180
76 accacaagct	tggcttcagg	ccaagccag	ccaggggcca	gggtggagga	aagtccatcc	240
77 ggagtctgca	tggccagctg	ggagaccctg	gggctcaatt	tccccatctg	tggagccgct	300
78 atgaccagct	gacaccccttc	acctccgcta	ctgcatggcc	ctgtgccata	ggtgctaggg	360
79 agcaaatggg	gggaggcagg	agagaaagag	ccccacttct	caggcctggg	gggctgcccc	420
80 actgtcctgt	tcccacagtc	cccactgtgt	ctcagcacaa	ggacactgac	aggggtggga	480
81 ggggatctga	ccctcaaccc	gccttccacc	caaaggcccc	gggctgaccc	cctccccc	540
82 cctcccccgtc	agggatgctg	accatcaactg	acttcatcc	ggtgctgcat	cgctactaca	600
83 ggtccccccct	ggtgaggagt	gggctgggaa	tcttatggc	acccagagg	gcggggcgg	660
84 aggggagtc	tcctggagcc	ttgtgcccta	gaagccacg	tcttcgtac	ttctggagtc	720
85 ctgtcgatgt	ctctaggtcc	agatctatga	gattgaacaa	cataagattt	agacctggag	780
86 ggtgagtg	ggagaggaac	ccggaaagg	gctgtggtg	atggtggggc	agggcttaag	840
87 gtggaggatg	ggcagtgggg	atgtcctgg	gtgaacaggg	gagggacaat	aggagccctg	900
88 ggtgcctgac	ggaagggaag	ctgcctggg	ctgcaaggtg	aggcaggtg	ccggctcccc	960
89 tggcctgact	ctggctctt	ctgcagagat	ctacctgca	gctgcttca	agcctcttgt	1020
90 ctccatctct	cctaattgata	ggtgggtgtc	tctgctcatt	cacctgagcc	tcctccccc	1080
91 acagtccccct	tcccccgtcc	cactcagctc	tgaactcacc	tcttcatcc	aggcggcaca	1140
92 cagacaagg	agccttgg	ccctgcctc	cttttaggg	gcctggatg	gaggttgtct	1200
93 ctccctaggc	tgccccgagg	ctcaactgctc	ccatctctgc	agcctgttt	aagctgtcta	1260
94 caccctcatc	aagaaccgg	ccatcgcc	gcctgttctt	gaccgggt	caggcaacgt	1320
95 actccacatc	ctcacacaca	aacgcctgct	caagttctg	cacatcttt	taagctgg	1380
96 cccaggtgg	aggaagggg	agacctggg	aggtgatcg	agggcctgag	gagtottcag	1440
97 ccctagcgt	cgtggggaa	agctgggagc	cctcttgaag	ctgctggatc	cctgatctcc	1500
98 acctggtccc	catcctaacc	agggttccct	gctgccccgg	ccctccccc	tctaccgcac	1560
99 tatccaagat	ttgggcatcg	gcacattccg	agactggct	gtgggtctgg	agacagcacc	1620
100 catcctgact	gcactggaca	tcttggat	ccggcgtgt	tctgcactgc	ctgtggtcaa	1680
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111	ttcccgctt	gatgtgattg	taagtgtcgc	tggaaaggtg	ggatgctgca	ggaggctaa	120
112	gggtgtggg	atgggtggg	ggcctctgt	gaccagggg	accttgacaa	gtatgcaggg	180
113	gttgacatct	gttagggtagg	agcccagca	agggggtgac	taggagccat	acttctct	240
114	ctgccccagc	acctggctgc	ccagcaaacc	tacaaccacc	tggacatgag	tgtggagaa	300
115	gccctgaggg	agaggacact	atgtctggag	ggagtcctt	cctgccagcc	ccacgagagc	360
116	ttgggggaag	tgatcgacag	gattgctcg	gagcaggtac	cgtgtccct	ccattcatgc	420
117	ccccaaacaca	tatacccag	tccttctcat	gcacggctcc	agccatccct	gaacatcggg	480
118	cacctggct	atccttccat	ttcatgacca	actcctggt	cccacactgg	cctgcacctg	540
119	gtcctgtcca	tggggccctt	atgccagggg	tcactgcca	ctgatcacct	tagccggc	600
120	acaccatccc	taactggtt	ctaggagacg	ctctctccct	cagtcatgtt	gggttgttc	660
121	ccctgattct	tggcaccaac	ctcagtagct	gctgtagccc	catggctctg	ccccctcact	720
122	gaacattgcg	gaccacagg	tacacagct	ggtgctagtg	gacgagaccc	agcatcttt	780
123	gggcgtggc	tccctctccg	acatcctca	ggcactggtg	ctcagccctg	ctggcatcga	840
124	tgcctcggg	gcctgagaag	atctgagttc	tcaatccaa	gccacctgca	cacctggaag	900
125	ccaatgaagg	gaactggaga	actcagcctt	catcttcccc	caccccccatt	tgctggttca	960
126	gctatgattc	agtaggctc	tgcctcggtc	catgacacca	gccttttagt	cttc	1014
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139			Met Glu Pro	Gly Leu Glu His	Ala Ala Leu	Arg Arg	
140			1	5	10		
142	acc cct tcc	tgg agc agc	ctt ggg ggt	tct gag cat	caa gag atg	agc	100
143	Thr Pro Ser	Trp Ser Ser	Leu Gly	Gly Ser Glu His	Gln Glu Met	Ser	
144			15	20	25		
146	ttc cta gag	caa gaa aac	agc agc	tca tgg cca	tca cca gct	gtg acc	148
147	Phe Leu Glu	Gln Glu Asn	Ser Ser	Ser Trp Pro	Ser Pro Ala	Val Thr	
148			30	35	40		
150	agc agc tca	gaa aga atc	cgt ggg	aaa cgg agg	gcc aaa gcc	ttg aga	196
151	Ser Ser Glu	Arg Ile Arg	Gly Lys	Arg Arg Ala	Lys Ala	Leu Arg	
152			45	50	55		
154	tgg aca agg	cag aag tcg	gtg gag	gaa ggg gag	cca cca ggt	cag ggg	244
155	Trp Thr Arg	Gln Lys Ser	Val Glu	Gly Glu Pro	Pro Gly Gln	Gly	
156			60	65	70	75	
159	gaa ggt ccc	cgg tcc agg	cca gct	gct gag tcc	acc ggg ctg	gag gcc	292
160	Glu Gly Pro	Arg Ser Arg	Pro Ala	Ala Glu Ser	Thr Gly Leu	Glu Ala	
161			80	85	90		
163	aca ttc ccc	aag acc aca	ccc ttg	gct caa gct	gat cct gcc	ggg gtt	340
164	Thr Phe Pro	Lys Thr Pro	Leu Ala	Gln Ala Asp	Pro Ala	Gly Val	
165			95	100	105		
167	ggc act cca	cca aca ggg	tgg gac	tgc ctc ccc	tct gac tgt	aca gcc	388
168	Gly Thr Pro	Pro Thr Gly	Trp Asp	Cys Leu Pro	Ser Asp Cys	Thr Ala	
169			110	115	120		
171	tca gct gca	ggc tcc agc	aca gat	gat gtg gag	ctg gcc acg	gag ttc	436

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172	Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe			
173	125	130	135	
175	cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg gaa gag	484		
176	Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Gly Leu Leu Glu Glu			
177	140	145	150	155
179	agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag ctg ggc	532		
180	Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly			
181	160	165	170	
183	tgg gat gac gaa ctg cggtt aaaa ccc ggc gcc cag atc tac atg cgc ttc	580		
184	Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met Arg Phe			
185	175	180	185	
187	atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc aag cta	628		
188	Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys Leu			
189	190	195	200	
191	gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gct ctg	676		
192	Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala Leu			
193	205	210	215	
195	gtg gcc aac ggt gtg cggtt aaaa ccc ggc cct cta tgg gac agc aag aag cag	724		
196	Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln			
197	220	225	230	235
199	agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg ctg cat	772		
200	Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu His			
201	240	245	250	
203	cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa caa cat	820		
204	Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His			
205	255	260	265	
207	aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc aag cct	868		
208	Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro			
209	270	275	280	
212	ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc tac acc	916		
213	Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr			
214	285	290	295	
216	ctc atc aag aac cggtt aaaa ccc ggc ctg cct gtt ctt gac ccg gtg tca	964		
217	Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val Ser			
218	300	305	310	315
220	gac aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag ttc ctg	1012		
221	Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu			
222	320	325	330	
224	cac atc ttt ggt tcc ctg ctg ccc cggtt aaaa ccc tcc ttc ctc tac cgc act	1060		
225	His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr			
226	335	340	345	
228	atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg gtg ctg	1108		
229	Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu			
230	350	355	360	
232	gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac ccg cgt	1156		
233	Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg			
234	365	370	375	
236	gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg ggc ctc	1204		
237	Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val Gly Leu			

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240	tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc tac aac				1252
241	Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr Asn				
242	400	405	410		
244	cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta tgt				1300
245	His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu Cys				
246	415	420	425		
248	ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa gtg				1348
249	Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu Val				
250	430	435	440		
252	atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg gac				1396
253	Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val Asp				
254	445	450	455		
256	gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt cag				1444
257	Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln				
258	460	465	470	475	
260	gca ctg ctc agc cct gct ggc atc gat gcc ctc ggg gcc				1486
261	Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala				
262	480	485			
265	tgagaagatc tgagtccatca atcccaagcc acctgcacac ctggaaagcca atgaaggaa				1546
266	ctggagaact cagccatcat cttccccac ccccatattgc tggttcagct atgattcagg				1606
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278	20	25	30		
279	Asn Ser Ser Ser Trp Pro Ser Pro Ala Val Thr Ser Ser Ser Glu Arg				
280	35	40	45		
281	Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg Trp Thr Arg Gln Lys				
282	50	55	60		
283	Ser Val Glu Glu Gly Glu Pro Pro Gly Gln Gly Glu Gly Pro Arg Ser				
284	65	70	75	80	
285	Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala Thr Phe Pro Lys Thr				
286	85	90	95		
287	Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val Gly Thr Pro Pro Thr				
288	100	105	110		
289	Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala Ser Ala Ala Gly Ser				
290	115	120	125		
291	Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe Pro Ala Thr Glu Ala				
292	130	135	140		
293	Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu Arg Pro Ala Leu Cys				
294	145	150	155	160	
295	Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly Trp Asp Asp Glu Leu				
296	165	170	175		

VERIFICATION SUMMARY

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